

Association mapping, patterns of linkage disequilibrium and selection in the vicinity of the PHYTOCHROME C gene in pearl millet

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Key message Linkage analysis confirmed the association in the region of PHYC in pearl millet. The comparison of genes found in this region suggests that PHYC is the best candidate. Abstract Major efforts are currently underway to dissect the phenotype-genotype relationship in plants and animals using existing populations. This method exploits historical recombinations accumulated in these populations. However, linkage disequilibrium sometimes extends over a relatively long distance, particularly in genomic regions containing polymorphisms that have been targets for selection. In this case, many genes in the region could be statistically associated with the trait shaped by the selected polymorphism. Statistical analyses could help in identifying the best candidate genes into such a region where an association is found. In a previous study, we proposed that a fragment of the PHYTOCHROME C gene (PHYC) is associated with flowering time and morphological variations in pearl millet. In the present study, we first performed linkage analyses using three pearl millet F2 families to confirm the presence of a QTL in the vicinity of PHYC. We then analyzed a wider genomic region of ~100 kb around PHYC to pinpoint the gene that best explains the association with the trait in this region. A panel of 90 pearl millet inbred lines was used to assess the association. We used a Markov chain Monte Carlo approach to compare 75 markers distributed along this 100-kb region. We found the best candidate markers on the PHYC gene. Signatures of selection in this region were assessed in an independent data set and pointed to the same gene. These results foster confidence in the likely role of PHYC in phenotypic variation and encourage the development of functional studies.

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